

SEQUENCE LISTING

<110> Christensen, Bjorn Eggert
Mollgaard, Henrik
Kaasgaard, Svend
Lehmbeck, Jan

<120> Methods for producing polypeptides in
aspergillus mutant cells

<130> 4483.200-US

<140> 09/472,364

<141> 1999-12-23

<150> 60/139,593

<151> 1999-06-17

<150> 60/117,396

<151> 1999-01-27

<150> PA 1999 00745

<151> 1999-05-27

<150> PA 1998 01726

<151> 1998-12-23

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1393

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 5956

<221> CDS

<222> (15)...(1328)

<400> 1

ccgaaagctg agca atg gag atc tcc aag aaa gca gca aca ctg ctg cca	50
Met Glu Ile Ser Lys Lys Ala Ala Thr Leu Leu Pro	
1 5 10	

aag ccc ttc tac gtg ctg agt caa gcc ctg aac ctc tcg aac aag gac	98
Lys Pro Phe Tyr Val Leu Ser Gln Ala Leu Asn Leu Ser Asn Lys Asp	
15 20 25	

cac aca aaa tgg tgg tat agc aca gct ccg atg ttt gcc acc atg atg	146
His Thr Lys Trp Trp Tyr Ser Thr Ala Pro Met Phe Ala Thr Met Met	
30 35 40	

gcg ggg gcc ggc tat gat gtt cac gca cag tac aag ttc ctc tgt atc Ala Gly Ala Gly Tyr Asp Val His Ala Gln Tyr Lys Phe Leu Cys Ile 45 50 55 60	194
cac cgt gag gtc atc atc ccg gcg ttg ggt cca tac cca gaa aag ggt His Arg Glu Val Ile Ile Pro Ala Leu Gly Pro Tyr Pro Glu Lys Gly 65 70 75	242
cag ccc atg cac tgg aag agt cat ctc aca cgc ttc gga ctt cct ttc Gln Pro Met His Trp Lys Ser His Leu Thr Arg Phe Gly Leu Pro Phe 80 85 90	290
gag ctg agc ttc aat tac tcc aaa tca cta cta cgg ttt gca ttc gag Glu Leu Ser Phe Asn Tyr Ser Lys Ser Leu Leu Arg Phe Ala Phe Glu 95 100 105	338
ccc ctc ggt tcc ctg acg gga acg aag gat gat cca ttc aac acc cag Pro Leu Gly Ser Leu Thr Gly Thr Lys Asp Asp Pro Phe Asn Thr Gln 110 115 120	386
gca atc agg cct gtt ctc cag gac ctc aag gcc atg gtt cca ggg ctt Ala Ile Arg Pro Val Leu Gln Asp Leu Lys Ala Met Val Pro Gly Leu 125 130 135 140	434
gac ctg gaa tgg ttc gat cat ttc act aaa gca ttg gtc gtt tcg gag Asp Leu Glu Trp Phe Asp His Phe Thr Lys Ala Leu Val Val Ser Glu 145 150 155	482
gaa gag gct cgg act ctg cta gat cga gat att gag atc ccc gtc ttc Glu Glu Ala Arg Thr Leu Leu Asp Arg Asp Ile Glu Ile Pro Val Phe 160 165 170	530
aag aca cag aac aaa ctg gca gcc gat ctg gag cca tct ggc gat att Lys Thr Gln Asn Lys Leu Ala Ala Asp Leu Glu Pro Ser Gly Asp Ile 175 180 185	578
gtc ttg aag acc tac atc tac ccg cgg atc aag tcg atc gcg acc ggg Val Leu Lys Thr Tyr Ile Tyr Pro Arg Ile Lys Ser Ile Ala Thr Gly 190 195 200	626
acc cca aaa gag aga ctc atg ttt gac gca atc aag gct gcc gac aag Thr Pro Lys Glu Arg Leu Met Phe Asp Ala Ile Lys Ala Ala Asp Lys 205 210 215 220	674
ttt ggc aaa gtt gcc act cca ctg gca atc ctc gag gag ttt ata gct Phe Gly Lys Val Ala Thr Pro Leu Ala Ile Leu Glu Glu Phe Ile Ala 225 230 235	722
gag cga gca ccc acc ctc ctc ggc cac ttt ctc tca tgc gat ttg gtc Glu Arg Ala Pro Thr Leu Leu Gly His Phe Leu Ser Cys Asp Leu Val 240 245 250	770
aag ccg tcc gag tcc cga atc aag gtc tac tgt atg gaa cgc cag ctc Lys Pro Ser Glu Ser Arg Ile Lys Val Tyr Cys Met Glu Arg Gln Leu 255 260 265	818
gac ctg gcc tcc atc gaa ggt att tgg act ctc aac ggg cga cgg aac	866

Asp	Leu	Ala	Ser	Ile	Glu	Gly	Ile	Trp	Thr	Leu	Asn	Gly	Arg	Arg	Asn		
270						275					280						
gat cca gag aca ctg gat ggt ctg gat gcg ctg agg gag ctg tgg cag 914																	
Asp	Pro	Glu	Thr	Leu	Asp	Gly	Leu	Asp	Ala	Leu	Arg	Glu	Leu	Trp	Gln		
285					290				295					300			
cta ttg ccc gtc acg gag ggt ctg tgt cca ctg ccg aac tgc ttt tac 962																	
Leu	Leu	Pro	Val	Thr	Glu	Gly	Leu	Cys	Pro	Leu	Pro	Asn	Cys	Phe	Tyr		
				305				310						315			
gag ccg ggt acc tca ccg cag gag cag ctc ccc ttc att ata aat ttt 1010																	
Glu	Pro	Gly	Thr	Ser	Pro	Gln	Glu	Gln	Leu	Pro	Phe	Ile	Ile	Asn	Phe		
			320				325						330				
acc ttg tct cct aaa agc gca ctt ccc gaa cca cag atc tat ttc cct 1058																	
Thr	Leu	Ser	Pro	Lys	Ser	Ala	Leu	Pro	Glu	Pro	Gln	Ile	Tyr	Phe	Pro		
		335					340					345					
gct ttt ggg cag aac gac aaa acc atc gcg gaa gga ttg gcc acc ttc 1106																	
Ala	Phe	Gly	Gln	Asn	Asp	Lys	Thr	Ile	Ala	Glu	Gly	Leu	Ala	Thr	Phe		
	350				355						360						
ttt gag agc aga ggt tgg ggt ggc ttg gct aag agc tat cca gcg gat 1154																	
Phe	Glu	Ser	Arg	Gly	Trp	Gly	Gly	Leu	Ala	Lys	Ser	Tyr	Pro	Ala	Asp		
365					370				375					380			
ttg gca tcc tac tat ccc gat gtg gac ctg cag acc gca aat cac ctg 1202																	
Leu	Ala	Ser	Tyr	Tyr	Pro	Asp	Val	Asp	Leu	Gln	Thr	Ala	Asn	His	Leu		
				385				390						395			
cag gcg tgg atc tcc ttc tct tac aag ggg aaa aaa ccg tac atg agt 1250																	
Gln	Ala	Trp	Ile	Ser	Phe	Ser	Tyr	Lys	Gly	Lys	Lys	Pro	Tyr	Met	Ser		
		400					405					410					
gtg tac ctc cat acc ttc gaa gcg ttc agt gct gct gcc cag gag gtg 1298																	
Val	Tyr	Leu	His	Thr	Phe	Glu	Ala	Phe	Ser	Ala	Ala	Ala	Gln	Glu	Val		
	415					420					425						
gct atg tgt cac gat ggc cac aat cct tag gactagttta tcccttcatt 1348																	
Ala	Met	Cys	His	Asp	Gly	His	Asn	Pro	*								
430					435												
ctatgcatcc gttgaatgtg ttggtcgaaa aaaaaaaaaa aaaaa 1393																	

<210> 2

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Primer 5956

<400> 2

Met	Glu	Ile	Ser	Lys	Lys	Ala	Ala	Thr	Leu	Leu	Pro	Lys	Pro	Phe	Tyr		
1				5					10					15			
Val	Leu	Ser	Gln	Ala	Leu	Asn	Leu	Ser	Asn	Lys	Asp	His	Thr	Lys	Trp		

			20					25					30				
Trp	Tyr	Ser	Thr	Ala	Pro	Met	Phe	Ala	Thr	Met	Met	Ala	Gly	Ala	Gly		
		35					40					45					
Tyr	Asp	Val	His	Ala	Gln	Tyr	Lys	Phe	Leu	Cys	Ile	His	Arg	Glu	Val		
	50					55					60						
Ile	Ile	Pro	Ala	Leu	Gly	Pro	Tyr	Pro	Glu	Lys	Gly	Gln	Pro	Met	His		
65					70					75					80		
Trp	Lys	Ser	His	Leu	Thr	Arg	Phe	Gly	Leu	Pro	Phe	Glu	Leu	Ser	Phe		
			85						90					95			
Asn	Tyr	Ser	Lys	Ser	Leu	Leu	Arg	Phe	Ala	Phe	Glu	Pro	Leu	Gly	Ser		
		100						105					110				
Leu	Thr	Gly	Thr	Lys	Asp	Asp	Pro	Phe	Asn	Thr	Gln	Ala	Ile	Arg	Pro		
	115						120					125					
Val	Leu	Gln	Asp	Leu	Lys	Ala	Met	Val	Pro	Gly	Leu	Asp	Leu	Glu	Trp		
	130					135					140						
Phe	Asp	His	Phe	Thr	Lys	Ala	Leu	Val	Val	Ser	Glu	Glu	Glu	Ala	Arg		
145					150					155					160		
Thr	Leu	Leu	Asp	Arg	Asp	Ile	Glu	Ile	Pro	Val	Phe	Lys	Thr	Gln	Asn		
			165						170					175			
Lys	Leu	Ala	Ala	Asp	Leu	Glu	Pro	Ser	Gly	Asp	Ile	Val	Leu	Lys	Thr		
		180						185					190				
Tyr	Ile	Tyr	Pro	Arg	Ile	Lys	Ser	Ile	Ala	Thr	Gly	Thr	Pro	Lys	Glu		
	195					200						205					
Arg	Leu	Met	Phe	Asp	Ala	Ile	Lys	Ala	Ala	Asp	Lys	Phe	Gly	Lys	Val		
	210					215					220						
Ala	Thr	Pro	Leu	Ala	Ile	Leu	Glu	Glu	Phe	Ile	Ala	Glu	Arg	Ala	Pro		
225					230					235					240		
Thr	Leu	Leu	Gly	His	Phe	Leu	Ser	Cys	Asp	Leu	Val	Lys	Pro	Ser	Glu		
			245						250					255			
Ser	Arg	Ile	Lys	Val	Tyr	Cys	Met	Glu	Arg	Gln	Leu	Asp	Leu	Ala	Ser		
		260						265					270				
Ile	Glu	Gly	Ile	Trp	Thr	Leu	Asn	Gly	Arg	Arg	Asn	Asp	Pro	Glu	Thr		
	275					280						285					
Leu	Asp	Gly	Leu	Asp	Ala	Leu	Arg	Glu	Leu	Trp	Gln	Leu	Leu	Pro	Val		
	290					295					300						
Thr	Glu	Gly	Leu	Cys	Pro	Leu	Pro	Asn	Cys	Phe	Tyr	Glu	Pro	Gly	Thr		
305					310					315					320		
Ser	Pro	Gln	Glu	Gln	Leu	Pro	Phe	Ile	Ile	Asn	Phe	Thr	Leu	Ser	Pro		
			325						330					335			
Lys	Ser	Ala	Leu	Pro	Glu	Pro	Gln	Ile	Tyr	Phe	Pro	Ala	Phe	Gly	Gln		
		340						345					350				
Asn	Asp	Lys	Thr	Ile	Ala	Glu	Gly	Leu	Ala	Thr	Phe	Phe	Glu	Ser	Arg		
	355						360					365					
Gly	Trp	Gly	Gly	Leu	Ala	Lys	Ser	Tyr	Pro	Ala	Asp	Leu	Ala	Ser	Tyr		
	370					375					380						
Tyr	Pro	Asp	Val	Asp	Leu	Gln	Thr	Ala	Asn	His	Leu	Gln	Ala	Trp	Ile		
385					390					395					400		
Ser	Phe	Ser	Tyr	Lys	Gly	Lys	Lys	Pro	Tyr	Met	Ser	Val	Tyr	Leu	His		
			405						410					415			
Thr	Phe	Glu	Ala	Phe	Ser	Ala	Ala	Ala	Gln	Glu	Val	Ala	Met	Cys	His		
		420						425					430				
Asp	Gly	His	Asn	Pro													
		435															

<210> 3
 <211> 20
 <212> DNA

5956 5955 6120 6121

<213> Artificial Sequence

<220>

<223> Primer 5956

<400> 3

ggatccaggg ctccctggag

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 5955

<400> 4

cctgaccagc cagatctcct

20

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 6120

<400> 5

agtgagagaa ctccctcctc

20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 6121

<400> 6

ccatatcttc tcagtctcca

20